

B. Bunner

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/721,341

DATE: 08/27/2002

TIME: 10:54:51

#16

Input Set : N:\Crf3\RULE60\09721341.txt

Output Set: N:\CRF4\08272002\I721341.raw

3 <110> APPLICANT: Gosling, Jennifa  
4 Dairaghi, Daniel J.  
5 Hanley, Michael  
6 Miao, Zhenhua  
7 Schall, Thomas J.  
8 ChemoCentryx, Inc.  
10 <120> TITLE OF INVENTION: Chemokine Receptor  
12 <130> FILE REFERENCE: 019934-000710US  
14 <140> CURRENT APPLICATION NUMBER: 09/721,341  
15 <141> CURRENT FILING DATE: 2000-11-21  
17 <150> PRIOR APPLICATION NUMBER: US 09/686,020  
18 <151> PRIOR FILING DATE: 2000-10-10  
20 <150> PRIOR APPLICATION NUMBER: US 60/159,015  
21 <151> PRIOR FILING DATE: 1999-10-12  
23 <150> PRIOR APPLICATION NUMBER: US 60/159,210  
24 <151> PRIOR FILING DATE: 1999-10-13  
26 <150> PRIOR APPLICATION NUMBER: US 60/172,979  
27 <151> PRIOR FILING DATE: 1999-12-20  
29 <150> PRIOR APPLICATION NUMBER: US 60/173,388  
30 <151> PRIOR FILING DATE: 1999-12-28  
32 <150> PRIOR APPLICATION NUMBER: US 60/186,626  
33 <151> PRIOR FILING DATE: 2000-03-03  
35 <160> NUMBER OF SEQ ID NOS: 14  
37 <170> SOFTWARE: PatentIn Ver. 2.1  
39 <210> SEQ ID NO: 1  
40 <211> LENGTH: 1147  
41 <212> TYPE: DNA  
42 <213> ORGANISM: Homo sapiens  
44 <220> FEATURE:  
45 <221> NAME/KEY: CDS  
46 <222> LOCATION: (1)..(1053)  
48 <220> FEATURE:  
49 <223> OTHER INFORMATION: chemokine receptor (CCX CKR)  
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54 1 5 10 15  
56 gaa atg aat ggc act tat gac tac agt caa tat gaa ctg atc tgt atc 96  
57 Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile  
58 20 25 30  
60 aaa gaa gat gtc aga gaa ttt gca aaa gtt ttc ctc cct gta ttc ctc 144  
61 Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu  
62 35 40 45

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66 aca ata gtt ttc gtc att gga ctt gca ggc aat tcc atg gta gtg gca 192
67 Thr Ile Val Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala
68      50                      55                      60
70 att tat gcc tat tac aag aaa cag aga acc aaa aca gat gtg tac atc 240
71 Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile
72 65                      70                      75                      80
74 ctg aat ttg gct gta gca gat tta ctc ctt cta ttc act ctg cct ttt 288
75 Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Leu Phe Thr Leu Pro Phe
76                      85                      90                      95
78 tgg gct gtt aat gca gtt cat ggg tgg gtt tta ggg aaa ata atg tgc 336
79 Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys
80      100                      105                      110
82 aaa ata act tca gcc ttg tac aca cta aac ttt gtc tct gga atg cag 384
83 Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln
84      115                      120                      125
86 ttt ctg gct tgt atc agc ata gac aga tat gtg gca gta act aaa gtc 432
87 Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Lys Val
88      130                      135                      140
90 ccc agc caa tca gga gtg gga aaa cca tgc tgg atc atc tgt ttc tgt 480
91 Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys
92 145                      150                      155                      160
94 gtc tgg atg gct gcc atc ttg ctg agc ata ccc cag ctg gtt ttt tat 528
95 Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr
96      165                      170                      175
98 aca gta aat gac aat gct agg tgc att ccc att ttc ccc cgc tac cta 576
99 Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu
100      180                      185                      190
102 gga aca tca atg aaa gca ttg att caa atg cta gag atc tgc att gga 624
103 Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly
104      195                      200                      205
106 ttt gta gta ccc ttt ctt att atg ggg gtg tgc tac ttt atc aca gca 672
107 Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala
108      210                      215                      220
110 agg aca ctc atg aag atg cca aac att aaa ata tct cga ccc cta aaa 720
111 Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys
112 225                      230                      235                      240
114 gtt ctg ctc aca gtc gtt ata gtt ttc att gtc act caa ctg cct tat 768
115 Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr
116      245                      250                      255
118 aac att gtc aag ttc tgc cga gcc ata gac atc atc tac tcc ctg atc 816
119 Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile
120      260                      265                      270
122 acc agc tgc aac atg agc aaa cgc atg gac atc gcc atc caa gtc aca 864
123 Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr
124      275                      280                      285
128 gaa agc atc gca ctc ttt cac agc tgc ctc aac cca atc ctt tat gtt 912
129 Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val
130      290                      295                      300
132 ttt atg gga gca tct ttc aaa aac tac gtt atg aaa gtg gcc aag aaa 960

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133 Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys
134 305          310          315          320
136 tat ggg tcc tgg aga aga cag aga caa agt gtg gag gag ttt cct ttt 1008
137 Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe
138          325          330          335
140 gat tct gag ggt cct aca gag cca acc agt act ttt agc att taa 1053
141 Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile
142          340          345          350
144 aggtaaaaact gctctgcctt ttgcttggat acatatgaat gatgctttcc cctcaaataa 1113
146 aacatctgcc ttattctgaa aaaaaaaaaa aaam 1147
149 <210> SEQ ID NO: 2
150 <211> LENGTH: 350
151 <212> TYPE: PRT
152 <213> ORGANISM: Homo sapiens
W--> 153 <220> FEATURE:
154 <223> OTHER INFORMATION: chemokine receptor (CCX CKR)
156 <400> SEQUENCE: 2
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158 1          5          10          15
159 Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile
160          20          25          30
161 Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu
162          35          40          45
163 Thr Ile Val Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala
164          50          55          60
165 Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile
166 65          70          75          80
167 Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Leu Phe Thr Leu Pro Phe
168          85          90          95
169 Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys
170          100          105          110
171 Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln
172          115          120          125
173 Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Lys Val
174          130          135          140
175 Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys
176 145          150          155          160
177 Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr
178          165          170          175
179 Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu
180          180          185          190
181 Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly
182          195          200          205
183 Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala
184          210          215          220
185 Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys
186 225          230          235          240
187 Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr
188          245          250          255

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191 Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile
192          260          265          270
193 Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr
194          275          280          285
195 Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val
196          290          295          300
197 Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys
198 305          310          315          320
199 Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe
200          325          330          335
201 Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile
202          340          345          350
206 <210> SEQ ID NO: 3
207 <211> LENGTH: 1147
208 <212> TYPE: DNA
209 <213> ORGANISM: Homo sapiens
211 <220> FEATURE:
212 <223> OTHER INFORMATION: chemokine receptor (variant)
214 <400> SEQUENCE: 3
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216 actgatgact acagtcagta tgaactgac tgtatcaaag aagatgtcag agaatttgcc 120
217 aaagttttcc cccctgtatt cctcacaata gttttcgtca ttggacttgc aggcaattcc 180
218 atggtagtgg caatttatgc ctattacaag aaacagagaa ccaaaacaga tgtgtacatc 240
219 ctgaatttgg ctgtagcaga tttactcctt ctattcactc tgcctttttg ggctgttaat 300
220 gcagttcatg ggtgggtttt agggaaaata atgtgcaaaa taacttcagc cttgtacaca 360
221 ctaaactttg tctctggaat gcagtttctg gcttgtatca gcatagacag atatgtggca 420
222 gtaactaaag tccccagcca atcaggagtg ggaaaaccat gctggatcat ctgtttctgt 480
223 gtctggatgg ctgccatctt gctgagcata cccagctggg ttttttatac agtaaatac 540
224 aatgttaggt gcattcccat ttccccccgc aacttaggaa catcaatgaa agcattgatt 600
225 caaatgctag agatctgcat tggatttgta gtaccctttc ttattatggg ggtgtgtctac 660
226 tttatcacag caaggacact catgaagatg ccaaacatta aaatatctcg acccctaaaa 720
227 gttctgctca cagtcgttat agttttcatt gtcaactcaac tgccttataa cattgtcaag 780
228 ttctgcccag ccatagacat catctactcc ctgatcacca gctgcaacat gagcaaacgc 840
229 atggacatcg ccatccaagt cacagaaagc atcgcaactc ttcacagctg cctcaaccca 900
230 atccttttatg tttttatggg agcatctttc aaaaactacg ttatgaaagt ggccaagaaa 960
231 tatgggtcct ggagaagaca gagacaaagt gtggaggagt ttccttttga ttctgagggg 1020
232 cctacagagc caaccagtac ttttagcatt taaaggtaaa actgctctgc cttttgcttg 1080
233 gatacatatg aatgatgctt tccctcaaaa taaaacatct gccttattct gaaaaaaaaa 1140
234 aaaaaaam                                     1147
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238 <211> LENGTH: 25
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240 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
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252 <211> LENGTH: 19
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Input Set : N:\Crf3\RULE60\09721341.txt

Output Set: N:\CRF4\08272002\I721341.raw

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254 <213> ORGANISM: Artificial Sequence  
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257 <223> OTHER INFORMATION: Description of Artificial Sequence:primer  
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264 <211> LENGTH: 369  
265 <212> TYPE: PRT  
266 <213> ORGANISM: Homo sapiens  
268 <220> FEATURE:  
269 <223> OTHER INFORMATION: chemokine receptor (CCR9)  
271 <400> SEQUENCE: 6  
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273 1 5 10 15  
275 Tyr Gly Ser Glu Ser Thr Ser Ser Met Glu Asp Tyr Val Asn Phe Asn  
276 20 25 30  
278 Phe Thr Asp Phe Tyr Cys Glu Lys Asn Asn Val Arg Gln Phe Ala Ser  
279 35 40 45  
281 His Phe Leu Pro Pro Leu Tyr Trp Leu Val Phe Ile Val Gly Ala Leu  
282 50 55 60  
284 Gly Asn Ser Leu Val Ile Leu Val Tyr Trp Tyr Cys Thr Arg Val Lys  
285 65 70 75 80  
287 Thr Met Thr Asp Met Phe Leu Leu Asn Leu Ala Ile Ala Asp Leu Leu  
288 85 90 95  
290 Phe Leu Val Thr Leu Pro Phe Trp Ala Ile Ala Ala Ala Asp Gln Trp  
291 100 105 110  
293 Lys Phe Gln Thr Phe Met Cys Lys Val Val Asn Ser Met Tyr Lys Met  
294 115 120 125  
296 Asn Phe Tyr Ser Cys Val Leu Leu Ile Met Cys Ile Ser Val Asp Arg  
297 130 135 140  
299 Tyr Ile Ala Ile Ala Gln Ala Met Arg Ala His Thr Trp Arg Glu Lys  
300 145 150 155 160  
302 Arg Leu Leu Tyr Ser Lys Met Val Cys Phe Thr Ile Trp Val Leu Ala  
303 165 170 175  
305 Ala Ala Leu Cys Ile Pro Glu Ile Leu Tyr Ser Gln Ile Lys Glu Glu  
306 180 185 190  
308 Ser Gly Ile Ala Ile Cys Thr Met Val Tyr Pro Ser Asp Glu Ser Thr  
309 195 200 205  
313 Lys Leu Lys Ser Ala Val Leu Thr Leu Lys Val Ile Leu Gly Phe Phe  
314 210 215 220  
316 Leu Pro Phe Val Val Met Ala Cys Cys Tyr Thr Ile Ile Ile His Thr  
317 225 230 235 240  
319 Leu Ile Gln Ala Lys Lys Ser Ser Lys His Lys Ala Leu Lys Val Thr  
320 245 250 255  
322 Ile Thr Val Leu Thr Val Phe Val Leu Ser Gln Phe Pro Tyr Asn Cys  
323 260 265 270  
325 Ile Leu Leu Val Gln Thr Ile Asp Ala Tyr Ala Met Phe Ile Ser Asn  
326 275 280 285

VERIFICATION SUMMARY

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